

## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:27:47 ; Search time 42 Seconds  
(without alignments)  
58.653 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: 1 KNESTNATNTKQWRDETKGPRDEAKRKNKTAG 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/ECTUS\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 55    | 31.2        | 72     | US-09-328-352-6545  | Sequence 6545, Ap  |
| 2          | 55    | 31.2        | 471    | US-09-106-464-2     | Sequence 2, Appli  |
| 3          | 53    | 30.1        | 277    | US-09-134-000C-4173 | Sequence 4173, Ap  |
| 4          | 52    | 29.5        | 75     | US-09-543-681A-7857 | Sequence 7857, Ap  |
| 5          | 51.5  | 29.3        | 1094   | US-09-268-347-32    | Sequence 32, Appli |
| 6          | 51    | 29.0        | 165    | US-08-965-689A-3    | Sequence 3, Appli  |
| 7          | 51    | 29.0        | 165    | US-09-359-967-3     | Sequence 3, Appli  |
| 8          | 51    | 29.0        | 165    | US-09-538-092-1224  | Sequence 1224, Ap  |
| 9          | 51    | 29.0        | 165    | US-09-949-016-6345  | Sequence 6345, Ap  |
| 10         | 51    | 29.0        | 166    | US-08-918-723-4     | Sequence 4, Appli  |
| 11         | 51    | 29.0        | 166    | US-09-237-507-4     | Sequence 4, Appli  |
| 12         | 51    | 29.0        | 176    | US-09-949-016-8150  | Sequence 8150, Ap  |
| 13         | 51    | 29.0        | 238    | US-09-377-285B-2    | Sequence 2, Appli  |
| 14         | 51    | 29.0        | 354    | US-09-377-285B-4    | Sequence 4, Appli  |
| 15         | 51    | 29.0        | 354    | US-09-377-285B-26   | Sequence 26, Appli |
| 16         | 51    | 29.0        | 354    | US-09-377-285B-36   | Sequence 36, Appli |
| 17         | 51    | 29.0        | 366    | US-09-377-285B-38   | Sequence 38, Appli |
| 18         | 51    | 29.0        | 455    | US-09-130-339-2     | Sequence 2, Appli  |
| 19         | 50    | 28.4        | 96     | US-09-621-976-7575  | Sequence 7575, Ap  |
| 20         | 50    | 28.4        | 106    | US-09-621-976-7576  | Sequence 7576, Ap  |
| 21         | 50    | 28.4        | 106    | US-09-621-976-7577  | Sequence 7577, Ap  |
| 22         | 50    | 28.4        | 106    | US-09-621-976-7578  | Sequence 7578, Ap  |
| 23         | 50    | 28.4        | 198    | US-09-270-767-36571 | Sequence 36571, A  |
| 24         | 50    | 28.4        | 198    | US-09-270-767-51788 | Sequence 51788, A  |
| 25         | 50    | 28.4        | 476    | US-09-673-300-10    | Sequence 10, Appli |
| 26         | 50    | 28.4        | 501    | US-09-902-540-11195 | Sequence 11195, A  |
| 27         | 48.5  | 27.6        | 220    | US-09-052-089A-4    | Sequence 4, Appli  |

ALIGNMENTS

RESULT 1

US-09-328-352-6545  
; Sequence 6545, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328.352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 6545  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-6545

Query Match 31.2%; Score 55; DB 4; Length 72;  
Best Local Similarity 48.0%; Fred. NO. 0.9;  
Matches 12; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 6 TNATNTKQWRDETKGPF-----RDEAK 26  
DB 3 SNTGTGVKWFNETKGFGFIQTDEGK 27

RESULT 2

US-09-106-464-2  
; Sequence 2, Application US/09106464  
; Patent No. 6011145  
; GENERAL INFORMATION:  
; APPLICANT: Steffens, John C.  
; APPLICANT: Ghangas, Gurdev S.  
; APPLICANT: Kuai, Jian-Ping  
; APPLICANT: Rannetta, Nancy  
; TITLE OF INVENTION: Chain Length Specific UDP-Glc:Fatty Acid  
; FILE REFERENCE: Glucosyltransferases  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Jones, Tullar & Cooper, P.C.  
; STREET: P.O. Box 2266 Eads Station  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/106,464
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/055,554
/ FILING DATE: 13-AUG-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Spector, Eric S.
/ REGISTRATION NUMBER: 22495
/ TELEPHONE: 703-415-1500
/ TELEFAX: 703-415-1508
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 471 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-106-464-2

Query Match 31.2%; Score 55; DB 3; Length 471;
Best Local Similarity 37.5%; Pred. No. 7.9;
Matches 12; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 KNESTNATNTKQWRDETKGRDEAKRFKNTA 32
Db 415 KREATAIKRVASEETEGFRSRAKEYKEMA 446

RESULT 3
US-09-134-000C-4173
/ Sequence 4173, Application US/09134000C
/ Patent No. 6617156
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
/ ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 032796-032
/ CURRENT APPLICATION NUMBER: US/09/134,000C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/055,778
/ PRIOR FILING DATE: 1997-08-15
/ NUMBER OF SEQ ID NOS: 6812
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4173
/ LENGTH: 277
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
US-09-134-000C-4173

Query Match 30.1%; Score 53; DB 4; Length 277;
Best Local Similarity 34.6%; Pred. No. 8.3;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 7 NATNTKQWRDETKGRDEAKRFKNTA 32
Db 108 NEESTKEWQDTTIKEYQSESEKRRQSA 133

RESULT 4
US-09-543-681A-7857
/ Sequence 7857, Application US/09543681A
/ Patent No. 6605709
/ GENERAL INFORMATION:
/ APPLICANT: GARY BRETON
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
/ FILE REFERENCE: 2709.1002-001
/ CURRENT APPLICATION NUMBER: US/09/543,681A
/ CURRENT FILING DATE: 2000-04-05
/ PRIOR APPLICATION NUMBER: US 60/128,706
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/ PRIOR FILING DATE: 1999-04-09
/ NUMBER OF SEQ ID NOS: 8344
/ SEQ ID NO 7857
/ LENGTH: 75
/ TYPE: PRT
/ ORGANISM: Proteus mirabilis
US-09-543-681A-7857

Query Match 29.5%; Score 52; DB 4; Length 75;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 NESSTNATNTKQWRDETKGF 21
Db 4 NSMSNSMTGTVKWFDEGKGF 23

RESULT 5
US-09-268-347-32
/ Sequence 32, Application US/09268347
/ Patent No. 6335182
/ GENERAL INFORMATION:
/ APPLICANT: Loosmore, Sheena M.
/ TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
/ FILE REFERENCE: 1038-860
/ CURRENT APPLICATION NUMBER: US/09/268,347
/ CURRENT FILING DATE: 1999-03-16
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 32
/ LENGTH: 1094
/ TYPE: PRT
/ ORGANISM: Haemophilus influenzae
US-09-268-347-32

Query Match 29.3%; Score 51.5; DB 3; Length 1094;
Best Local Similarity 37.5%; Pred. No. 68;
Matches 12; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 3 ESSSTNATNTKQWRDETKGRDEAKRFKN-TAG 33
Db 365 ETVINAVNKAGWRIKTTGANNQAGQFETVTSG 396

RESULT 6
US-08-965-689A-3
/ Sequence 3, Application US/08965689A
/ Patent No. 6015702
/ GENERAL INFORMATION:
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/965,689A
/ FILING DATE: Herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/933,750
/ FILING DATE: September 23, 1997
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ENDANOT01
; CLONE: 2456290
US-08-965-689A-3

Query Match 29.0%; Score 51; DB 3; Length 165;
Best Local Similarity 38.5%; Pred. No. 8.9;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQWRDETKGFRDEAKR 27
Db 132 DESGANVDASKWRDDREQFYKIAKQ 157

RESULT 7
US-09-359-967-3
; Sequence 3, Application US/09359967
; Patent No. 6146624
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,967
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,689
; FILING DATE:
; APPLICATION NUMBER: 08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; LIBRARY: ENDANOT01
; CLONE: 2456290
US-09-359-967-3

Query Match 29.0%; Score 51; DB 3; Length 165;
Best Local Similarity 38.5%; Pred. No. 8.9;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQWRDETKGFRDEAKR 27
Db 132 DESGANVDASKWRDDREQFYKIAKQ 157

RESULT 8
US-09-538-092-1224
; Sequence 1224, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurafatSeqformatter Version 0.9
; SEQ ID NO 1224
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P56554
US-09-538-092-1224

Query Match 29.0%; Score 51; DB 4; Length 165;
Best Local Similarity 38.5%; Pred. No. 8.9;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQWRDETKGFRDEAKR 27
Db 132 DESGANVDASKWRDDREQFYKIAKQ 157

RESULT 9
US-09-949-016-6345
; Sequence 6345, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6345
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Human
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US-09-949-016-8150

Query Match 29.0%; Score 51; DB 4; Length 176;  
Best Local Similarity 38.5%; Pred. No. 9.6;  
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 2 NESSTNATNTKQRDETKGFRDEAKR 27

Db 143 DESGANVDASKWRDRDQFYKIAKQ 168

## RESULT 13

US-09-377-285B-2  
; Sequence 2, Application US/09377285B  
; Patent No. 6720175  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)  
; FILE REFERENCE: JHU1580-4  
; CURRENT APPLICATION NUMBER: US/09/377,285B  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-08-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-377-285B-2

Query Match 29.0%; Score 51; DB 4; Length 238;  
Best Local Similarity 33.3%; Pred. No. 14;  
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 7 NATNTKQRDETKGFRDEAKR 27

Db 204 STANVKQWKQQLAAYQEEAER 224

## RESULT 14

US-09-377-285B-4  
; Sequence 4, Application US/09377285B  
; Patent No. 6720175  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)  
; FILE REFERENCE: JHU1580-4  
; CURRENT APPLICATION NUMBER: US/09/377,285B  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494

; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-08-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-377-285B-4

Query Match 29.0%; Score 51; DB 4; Length 354;  
Best Local Similarity 33.3%; Pred. No. 22;  
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 7 NATNTKQRDETKGFRDEAKR 27

Db 204 STANVKQWKQQLAAYQEEAER 224

## RESULT 15

US-09-377-285B-26  
; Sequence 26, Application US/09377285B  
; Patent No. 6720175  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: WORLEY, Paul  
; APPLICANT: TU, Jian  
; APPLICANT: XIAO, Bo  
; APPLICANT: LEAHY, Daniel  
; APPLICANT: BENEKEN, Jutta  
; APPLICANT: LANAHAN, Anthony  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)  
; FILE REFERENCE: JHU1580-4  
; CURRENT APPLICATION NUMBER: US/09/377,285B  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/138,426  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,493  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/138,494  
; PRIOR FILING DATE: 1999-06-10  
; PRIOR APPLICATION NUMBER: US 60/097,334  
; PRIOR FILING DATE: 1998-08-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-377-285B-26

Query Match 29.0%; Score 51; DB 4; Length 354;  
Best Local Similarity 33.3%; Pred. No. 22;  
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 7 NATNTKQRDETKGFRDEAKR 27

Db 204 STANVKQWKQQLAAYQEEAER 224

Search completed: March 30, 2005, 14:38:44  
Job time : 43 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:31:07 ; Search time 138 Seconds  
(without alignments)  
79.176 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: 1 KNESTNATNTKQWRDETKGFRDEAKRFKNTAG 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*\*

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- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID               | Description        |
|------------|-------|-------------|--------|------------------|--------------------|
| 1          | 176   | 100.0       | 33     | US-10-444-662-8  | Sequence 8, Appli  |
| 2          | 176   | 100.0       | 33     | US-10-633-808-1  | Sequence 1, Appli  |
| 3          | 176   | 100.0       | 33     | US-10-633-808-22 | Sequence 22, Appli |
| 4          | 176   | 100.0       | 33     | US-10-633-808-23 | Sequence 23, Appli |
| 5          | 176   | 100.0       | 33     | US-10-633-808-36 | Sequence 36, Appli |
| 6          | 176   | 100.0       | 40     | US-10-633-808-16 | Sequence 16, Appli |
| 7          | 176   | 100.0       | 160    | US-10-633-808-5  | Sequence 5, Appli  |
| 8          | 176   | 100.0       | 309    | US-10-633-808-6  | Sequence 6, Appli  |
| 9          | 176   | 100.0       | 424    | US-10-633-808-7  | Sequence 7, Appli  |
| 10         | 176   | 100.0       | 573    | US-10-633-808-4  | Sequence 4, Appli  |
| 11         | 173   | 98.3        | 33     | US-10-633-808-14 | Sequence 14, Appli |
| 12         | 173   | 98.3        | 33     | US-10-633-808-15 | Sequence 15, Appli |
| 13         | 173   | 98.3        | 33     | US-10-782-075-7  | Sequence 7, Appli  |

|    |      |      |      |    |                      |                    |
|----|------|------|------|----|----------------------|--------------------|
| 14 | 172  | 97.7 | 33   | 15 | US-10-633-808-25     | Sequence 25, Appli |
| 15 | 167  | 94.9 | 33   | 15 | US-10-633-808-26     | Sequence 26, Appli |
| 16 | 167  | 94.9 | 33   | 15 | US-10-633-808-27     | Sequence 27, Appli |
| 17 | 165  | 93.8 | 31   | 15 | US-10-633-808-21     | Sequence 21, Appli |
| 18 | 165  | 93.8 | 33   | 15 | US-10-633-808-17     | Sequence 17, Appli |
| 19 | 160  | 90.9 | 30   | 15 | US-10-633-808-20     | Sequence 20, Appli |
| 20 | 156  | 88.6 | 29   | 15 | US-10-633-808-19     | Sequence 19, Appli |
| 21 | 152  | 86.4 | 28   | 15 | US-10-633-808-18     | Sequence 18, Appli |
| 22 | 150  | 85.2 | 28   | 15 | US-10-633-808-24     | Sequence 24, Appli |
| 23 | 150  | 85.2 | 28   | 15 | US-10-633-808-30     | Sequence 30, Appli |
| 24 | 147  | 83.5 | 27   | 15 | US-10-633-808-35     | Sequence 35, Appli |
| 25 | 141  | 80.1 | 33   | 15 | US-10-633-808-34     | Sequence 34, Appli |
| 26 | 134  | 76.1 | 25   | 15 | US-10-633-808-28     | Sequence 28, Appli |
| 27 | 134  | 76.1 | 25   | 15 | US-10-633-808-29     | Sequence 29, Appli |
| 28 | 121  | 68.8 | 22   | 15 | US-10-633-808-32     | Sequence 32, Appli |
| 29 | 79   | 44.9 | 15   | 15 | US-10-633-808-31     | Sequence 31, Appli |
| 30 | 56.5 | 32.1 | 3079 | 15 | US-10-369-493-2024   | Sequence 2024, Ap  |
| 31 | 56   | 31.8 | 154  | 15 | US-10-425-114-67327  | Sequence 67327, A  |
| 32 | 56   | 31.8 | 188  | 15 | US-10-866-527-62     | Sequence 60470, A  |
| 33 | 54.5 | 31.0 | 508  | 17 | US-10-866-527-62     | Sequence 62, Appli |
| 34 | 54   | 30.7 | 888  | 16 | US-10-437-963-118322 | Sequence 118322,   |
| 35 | 53.5 | 30.4 | 154  | 16 | US-10-437-963-105218 | Sequence 105218,   |
| 36 | 53.5 | 30.4 | 275  | 15 | US-10-424-599-226978 | Sequence 226978,   |
| 37 | 53.5 | 30.4 | 350  | 15 | US-10-425-114-65017  | Sequence 65017, A  |
| 38 | 53   | 30.1 | 553  | 15 | US-10-104-047-2655   | Sequence 2855, Ap  |
| 39 | 52.5 | 29.8 | 234  | 15 | US-10-369-493-11114  | Sequence 11114, A  |
| 40 | 52   | 29.5 | 175  | 15 | US-10-424-599-151075 | Sequence 151075,   |
| 41 | 52   | 29.5 | 205  | 15 | US-10-425-114-62679  | Sequence 62679, A  |
| 42 | 51   | 29.0 | 79   | 16 | US-10-767-701-45937  | Sequence 45937, A  |
| 43 | 51   | 29.0 | 145  | 16 | US-10-437-963-124570 | Sequence 124570,   |
| 44 | 51   | 29.0 | 148  | 14 | US-10-180-524-2      | Sequence 2, Appli  |
| 45 | 51   | 29.0 | 165  | 14 | US-10-157-669-17     | Sequence 17, Appli |

#### ALIGNMENTS

##### RESULT 1

US-10-444-662-8  
; Sequence 8, Application US/10444662  
; Publication No. US2003022026A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Rozema, David  
; APPLICANT: Wolff, Jon  
; APPLICANT: Wakefield, Darren  
; APPLICANT: Ekena, Kirk  
; APPLICANT: Hagstrom, James  
; TITLE OF INVENTION: Reversible Modification of Membrane Interaction  
; FILE REFERENCE: Mirus.035.01  
; CURRENT APPLICATION NUMBER: US/10/444,662  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 8  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-444-662-8

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESTNATNTKQWRDETKGFRDEAKRFKNTAG 33

DB 1 KNESTNATNTKQWRDETKGFRDEAKRFKNTAG 33

##### RESULT 2

US-10-633-808-1  
; Sequence 1, Application US/10633808  
; Publication No. US20040029826A1

GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex  
APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
FILE REFERENCE: Mirus.014.06  
CURRENT APPLICATION NUMBER: US/10/633,808  
CURRENT FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Bacteriophage T7  
US-10-633-808-1

*Current application*

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 3  
US-10-633-808-22  
Sequence 22, Application US/10633808  
Publication No. US20040029826A1  
GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex  
APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
FILE REFERENCE: Mirus.014.06  
CURRENT APPLICATION NUMBER: US/10/633,808  
CURRENT FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Bacteriophage T7  
US-10-633-808-22

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 4  
US-10-633-808-23  
Sequence 23, Application US/10633808  
Publication No. US20040029826A1  
GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex

APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
FILE REFERENCE: Mirus.014.06  
CURRENT APPLICATION NUMBER: US/10/633,808  
CURRENT FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 23  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Bacteriophage T7  
US-10-633-808-23

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 5  
US-10-633-808-36  
Sequence 36, Application US/10633808  
Publication No. US20040029826A1  
GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex  
APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
FILE REFERENCE: Mirus.014.06  
CURRENT APPLICATION NUMBER: US/10/633,808  
CURRENT FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 36  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Bacteriophage T7  
US-10-633-808-36

Query Match 100.0%; Score 176; DB 15; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 6  
US-10-633-808-16  
Sequence 16, Application US/10633808  
Publication No. US20040029826A1  
GENERAL INFORMATION:  
APPLICANT: Mirus Corporation  
APPLICANT: Wong, So  
APPLICANT: Wakefield, Darren  
APPLICANT: Sokoloff, Alex  
APPLICANT: Monahan, Sean  
APPLICANT: Sebestyen, Magdolna  
APPLICANT: Wolff, Jon  
APPLICANT: Higgs, Lori  
TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO

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; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-16

Query Match          100.0%; Score 176; DB 15; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.3e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33

RESULT 7
US-10-633-808-5
; Sequence 5, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdolna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-5

Query Match          100.0%; Score 176; DB 15; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
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Db 57 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 89

RESULT 8
US-10-633-808-6
; Sequence 6, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdolna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-6

Query Match          100.0%; Score 176; DB 15; Length 424;
Best Local Similarity 100.0%; Pred. No. 7e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
    |||||
Db 57 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 89

RESULT 9
US-10-633-808-7
; Sequence 7, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdolna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-7

Query Match          100.0%; Score 176; DB 15; Length 424;
Best Local Similarity 100.0%; Pred. No. 7e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
    |||||
Db 57 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 89

RESULT 10
US-10-633-808-4
; Sequence 4, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdolna
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-4
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Query Match 100.0%; Score 176; DB 15; Length 573;  
Best Local Similarity 100.0%; Pred. No. 9.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
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Db 206 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 238  
|||||

RESULT 11  
US-10-633-808-14  
; Sequence 14, Application US/10633808  
; Publication No. US20040029826A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Wong, So  
; APPLICANT: Wakefield, Darren  
; APPLICANT: Sokoloff, Alex  
; APPLICANT: Monahan, Sean  
; APPLICANT: Sebestyen, Magdolna  
; APPLICANT: Wolff, Jon  
; APPLICANT: Higgs, Lori  
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
; FILE REFERENCE: Mirus.014.06  
; CURRENT APPLICATION NUMBER: US/10/633,808  
; CURRENT FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-633-808-14

Query Match 98.3%; Score 173; DB 15; Length 33;  
Best Local Similarity 97.0%; Pred. No. 1.1e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
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Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 12  
US-10-633-808-15  
; Sequence 15, Application US/10633808  
; Publication No. US20040029826A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Wong, So  
; APPLICANT: Wakefield, Darren  
; APPLICANT: Sokoloff, Alex  
; APPLICANT: Monahan, Sean  
; APPLICANT: Sebestyen, Magdolna  
; APPLICANT: Wolff, Jon  
; APPLICANT: Higgs, Lori  
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
; FILE REFERENCE: Mirus.014.06  
; CURRENT APPLICATION NUMBER: US/10/633,808  
; CURRENT FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-633-808-15

Query Match 98.3%; Score 173; DB 15; Length 33;  
Best Local Similarity 97.0%; Pred. No. 1.1e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 13  
US-10-782-075-7  
; Sequence 7, Application US/10782075  
; Publication No. US20040167090A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Monahan, Sean  
; APPLICANT: Budker, Vladimir  
; APPLICANT: Nader, Lisa  
; APPLICANT: Subbotin, Vladimir  
; APPLICANT: Wolff, Jon A  
; TITLE OF INVENTION: Covalent Modification of RNA for In Vitro and In Vivo Delivery  
; FILE REFERENCE: Mirus.030.16.6  
; CURRENT APPLICATION NUMBER: US/10/782,075  
; CURRENT FILING DATE: 2004-02-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-782-075-7

Query Match 98.3%; Score 173; DB 16; Length 33;  
Best Local Similarity 97.0%; Pred. No. 1.1e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 14  
US-10-633-808-25  
; Sequence 25, Application US/10633808  
; Publication No. US20040029826A1  
; GENERAL INFORMATION:  
; APPLICANT: Mirus Corporation  
; APPLICANT: Wong, So  
; APPLICANT: Wakefield, Darren  
; APPLICANT: Sokoloff, Alex  
; APPLICANT: Monahan, Sean  
; APPLICANT: Sebestyen, Magdolna  
; APPLICANT: Wolff, Jon  
; APPLICANT: Higgs, Lori  
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO  
; FILE REFERENCE: Mirus.014.06  
; CURRENT APPLICATION NUMBER: US/10/633,808  
; CURRENT FILING DATE: 2003-08-04  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Bacteriophage T7  
US-10-633-808-25

Query Match 97.7%; Score 172; DB 15; Length 33;  
Best Local Similarity 97.0%; Pred. No. 1.5e-16;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 15  
US-10-633-808-26

```

; Sequence 26, Application US/10633808
; Publication No. US20040029826A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wong, So
; APPLICANT: Wakefield, Darren
; APPLICANT: Sokoloff, Alex
; APPLICANT: Monahan, Sean
; APPLICANT: Sebestyen, Magdalena
; APPLICANT: Wolff, Jon
; APPLICANT: Higgs, Lori
; TITLE OF INVENTION: A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO
; FILE REFERENCE: Mirus.014.06
; CURRENT APPLICATION NUMBER: US/10/633,808
; CURRENT FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Bacteriophage T7
US-10-633-808-26

Query Match      94.9%; Score 167; DB 15; Length 33;
Best Local Similarity 90.9%; Pred. No. 7.4e-16;
Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
       :|||||:|||||:|||||:|||||:|||||:
DB      1 RNESSTNATNTKQWRDETKGFRDEARRFNTAG 33

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Search completed: March 30, 2005, 14:41:09  
Job time : 139 secs

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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:14:33 ; Search time 170 Seconds  
(without alignments)  
75.077 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: 1 KNESTNATNTKQWRDETKGPRDEAKRFKNTAG 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description      |
|------------|-------|-------------|--------|----------|------------------|
| 1          | 176   | 100.0       | 33     | ADH51594 | Bacteriophage T7 |
| 2          | 176   | 100.0       | 33     | ADJ46278 | T7 phage         |
| 3          | 176   | 100.0       | 33     | ADJ46313 | T7 phage         |
| 4          | 176   | 100.0       | 40     | ADJ46293 | T7 phage         |
| 5          | 176   | 100.0       | 160    | ADJ46282 | T7 phage         |
| 6          | 176   | 100.0       | 309    | ADJ46283 | T7 phage         |
| 7          | 176   | 100.0       | 424    | ADJ46284 | T7 phage         |
| 8          | 176   | 100.0       | 573    | ADJ46281 | T7 phage         |
| 9          | 173   | 98.3        | 33     | ADJ46292 | T7 phage         |
| 10         | 173   | 98.3        | 33     | ADJ46291 | T7 phage         |
| 11         | 173   | 98.3        | 33     | ADJ46293 | T7 phage         |
| 12         | 172   | 97.7        | 33     | ADJ46302 | T7 phage         |
| 13         | 170   | 96.6        | 33     | ADJ46299 | T7 phage         |
| 14         | 170   | 96.6        | 33     | ADJ46300 | T7 phage         |
| 15         | 167   | 94.9        | 33     | ADJ46304 | T7 phage         |
| 16         | 167   | 94.9        | 33     | ADJ46303 | T7 phage         |
| 17         | 165   | 93.8        | 31     | ADJ46298 | T7 phage         |
| 18         | 165   | 93.8        | 33     | ADJ46294 | T7 phage         |
| 19         | 160   | 90.9        | 30     | ADJ46297 | T7 phage         |
| 20         | 156   | 88.6        | 29     | ADJ46296 | T7 phage         |
| 21         | 152   | 86.4        | 28     | ADJ46295 | T7 phage         |
| 22         | 150   | 85.2        | 28     | ADJ46301 | T7 phage         |
| 23         | 150   | 85.2        | 28     | ADJ46307 | T7 phage         |
| 24         | 147   | 83.5        | 27     | ADJ46312 | T7 phage         |
| 25         | 141   | 80.1        | 33     | ADJ46311 | T7 phage         |

|    |      |      |      |   |          |           |
|----|------|------|------|---|----------|-----------|
| 26 | 134  | 76.1 | 25   | 8 | ADJ46305 | T7 phage  |
| 27 | 134  | 76.1 | 25   | 8 | ADJ46306 | T7 phage  |
| 28 | 121  | 68.8 | 22   | 8 | ADJ46309 | T7 phage  |
| 29 | 79   | 44.9 | 15   | 8 | ADJ46308 | T7 phage  |
| 30 | 60   | 34.1 | 1460 | 3 | AAG40077 | Arabidops |
| 31 | 60   | 34.1 | 1462 | 3 | AAG40076 | Arabidops |
| 32 | 60   | 34.1 | 1518 | 3 | AAG40075 | Arabidops |
| 33 | 60   | 34.1 | 1604 | 3 | AAG31284 | Arabidops |
| 34 | 60   | 34.1 | 1606 | 3 | AAG31283 | Arabidops |
| 35 | 60   | 34.1 | 1662 | 3 | AAG31282 | Arabidops |
| 36 | 56.5 | 32.1 | 3079 | 8 | ADN19371 | Bacterial |
| 37 | 56   | 31.8 | 90   | 3 | AAG26831 | Zea mays  |
| 38 | 56   | 31.8 | 90   | 3 | AAG35425 | Zea mays  |
| 39 | 56   | 31.8 | 109  | 3 | AAG35424 | Zea mays  |
| 40 | 56   | 31.8 | 109  | 3 | AAG26830 | Zea mays  |
| 41 | 56   | 31.8 | 169  | 3 | AAG35423 | Zea mays  |
| 42 | 55   | 31.2 | 72   | 6 | ADA35258 | Acinetoba |
| 43 | 55   | 31.2 | 470  | 2 | AAW47172 | Glucosyl  |
| 44 | 55   | 31.2 | 470  | 2 | AAW06274 | Tomato de |
| 45 | 55   | 31.2 | 471  | 2 | AAW98009 | Medium-ch |

## ALIGNMENTS

RESULT 1  
ADH51594  
ID ADH51594 standard; peptide; 33 AA.  
XX  
AC ADH51594;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Bacteriophage T7 peptide related to reversible compound modification.  
XX  
KW amine-containing compound; membrane lipid; maleic anhydride;  
KW reversible modification; cross-linker; membrane activity;  
KW positive charge; toxicity.  
XX  
OS Enterobacteria phage T7.  
XX  
PN US2003220264-A1.  
XX  
PD 27-NOV-2003.  
XX  
PF 23-MAY-2003; 2003US-00444662.  
XX  
PR 24-MAY-2002; 2002US-0383298P.  
XX  
PA (ROZE/) ROZEMA D B.  
PA (WAKE/) WAKEFIELD D.  
PA (WOLF/) WOLFF J A.  
PA (EXEN/) EXENA K.  
PA (HAGS/) HAGSTROM J E.  
XX  
PI Rozema DB, Wakefield D, Wolff JA, Ekana K, Hagstrom JE;  
XX  
DR WPI; 2004-097358/10.  
XX  
PT Reversible modification of an amine-containing compound useful for  
XX delivering molecules to cells involves covalently attaching a substituted  
XX maleic anhydride to the amine.  
PS Example 12; SEQ ID NO 8; 17pp; English.  
XX  
CC This invention relates to a novel reversible modification of an amine-  
XX containing compound to alter interaction of the compound with membrane  
XX lipids which involves covalently attaching a substituted maleic anhydride  
XX to the amine. The invention is useful for reversible modification of an  
XX amine-containing compound for delivering molecules to cells and as cross-  
XX linkers. The modification of the compound inactivates its membrane  
XX activity, reduces its positive charge and toxicity and reverses its  
XX charge. The present sequence is that of a bacteriophage T7 peptide which

CC is related to the invention.

XX Sequence 33 AA;

Query Match 100.0%; Score 176; DB 8; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.1e-19;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

DB 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

RESULT 2

ADJ46278

ID ADJ46278 standard; peptide; 33 AA.

XX AC ADJ46278;

XX DT 06-MAY-2004 (first entry)

XX DE T7 p17 rod domain peptide, SEQ ID 1.

XX KW Hepatocyte delivery; T7; p17 rod domain.

XX OS Enterobacteria phage T7.

XX PN WO2004013307-A2.

XX PD 12-FEB-2004.

XX PF 04-AUG-2003; 2003WO-US024516.

XX PR 05-AUG-2002; 2002US-0401167P.

XX PR 04-AUG-2003; 2003US-00633808.

XX PA (MIRU-) MIRUS CORP.

XX PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;

XX PI Wakefield D, Sebestyen MG;

XX XWPI; 2004-203636/19.

XX Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to compound.

XX PS Claim 12; Page 2; 56pp; English.

XX The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (ADJ46278).

XX Sequence 33 AA;

Query Match 100.0%; Score 176; DB 8; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.1e-19;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

DB 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

RESULT 3

ADJ46313

ID ADJ46313 standard; peptide; 33 AA.

XX

AC ADJ46313;

XX DT 06-MAY-2004 (first entry)

XX DE T7 phase p17 protein ligand-related peptide, SEQ ID 36.

XX KW Hepatocyte delivery; T7; p17 rod domain.

XX OS Enterobacteria phage T7.

XX OS Synthetic.

XX FT Key Location/Qualifiers

XX FT Misc-difference 1..33

XX FT /note= "All D-form residues"

XX PN WO2004013307-A2.

XX PD 12-FEB-2004.

XX PF 04-AUG-2003; 2003WO-US024516.

XX PR 05-AUG-2002; 2002US-0401167P.

XX PR 04-AUG-2003; 2003US-00633808.

XX PA (MIRU-) MIRUS CORP.

XX PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;

XX PI Wakefield D, Sebestyen MG;

XX XWPI; 2004-203636/19.

XX Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to compound.

XX PS Disclosure; Page 10; 56pp; English.

XX The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-ADJ46313 are synthetic peptides derived from the T7 phase p17 protein ligand, where ADJ46291-ADJ46301 have amino acid changes which do not disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid changes which do disrupt hepatocyte targeting.

XX SQ Sequence 33 AA;

Query Match 100.0%; Score 176; DB 8; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.1e-19;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

DB 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33

RESULT 4

ADJ46293

ID ADJ46293 standard; peptide; 40 AA.

XX AC ADJ46293;

XX DT 06-MAY-2004 (first entry)

XX DE T7 phase p17 protein ligand, SEQ ID 16.

XX KW Hepatocyte delivery; T7; p17 rod domain.



OS Enterobacteria phage T7.  
OS Synthetic.  
XX WO2004013307-A2.  
XX 12-FEB-2004.  
XX 04-AUG-2003; 2003WO-US024516.  
XX 05-AUG-2002; 2002US-0401167P.  
XX 04-AUG-2003; 2003US-00633808.  
XX (MIRU-) MIRUS CORP.  
XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Luttke J, Higgs L;  
XX Wakefield D, Sebestyen MG;  
XX WPI; 2004-203636/19.  
XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
XX compound.  
XX Disclosure; Page 10; 56pp; English.  
XX The present invention relates to a composition (I) for delivering a  
XX therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
XX compound. In (I), the compound comprises a drug (interferon). (I)  
XX provides better hepatocyte specificity and potentially utilizes different  
XX cellular internalization pathways which allows more flexibility in  
XX designing delivery strategies and is useful for delivering therapeutic  
XX cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
XX p17 derived peptide, such as T7 p17 rod domain (ADJ46282). The present  
XX invention is the predicted sequence of a fragment of the T7 p17 protein.  
XX Sequence 160 AA;  
XX Query Match 100.0%; Score 176; DB 8; Length 160;  
XX Best Local Similarity 100.0%; Pred. No. 4.9e-18;  
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
DB 57 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 89  
RESULT 6  
ADJ46282  
ID ADJ46282 standard; protein; 309 AA.  
XX AC ADJ46282;  
XX 06-MAY-2004 (first entry)  
XX T7 p17 protein fragment 1-289, SEQ ID 6.  
XX Hepatocyte delivery; T7; p17 rod domain.  
XX Enterobacteria phage T7.  
XX WO2004013307-A2.  
XX 12-FEB-2004.  
XX 04-AUG-2003; 2003WO-US024516.  
XX 05-AUG-2002; 2002US-0401167P.  
XX 04-AUG-2003; 2003US-00633808.  
XX (MIRU-) MIRUS CORP.  
XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Luttke J, Higgs L;  
XX Wakefield D, Sebestyen MG;  
XX WPI; 2004-203636/19.  
XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
XX compound.  
XX Example 3; Page 26; 56pp; English.  
XX The present invention relates to a composition (I) for delivering a  
XX therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
XX compound. In (I), the compound comprises a drug (interferon). (I)  
XX provides better hepatocyte specificity and potentially utilizes different  
XX cellular internalization pathways which allows more flexibility in  
XX designing delivery strategies and is useful for delivering therapeutic  
XX cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
XX p17 derived peptide, such as T7 p17 rod domain (ADJ46282). The present  
XX invention is the predicted sequence of a fragment of the T7 p17 protein.  
XX Sequence 160 AA;  
XX Query Match 100.0%; Score 176; DB 8; Length 160;  
XX Best Local Similarity 100.0%; Pred. No. 4.9e-18;  
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
DB 57 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 89  
RESULT 6  
ADJ46282  
ID ADJ46282 standard; protein; 309 AA.  
XX AC ADJ46282;  
XX 06-MAY-2004 (first entry)  
XX T7 p17 protein fragment 1-289, SEQ ID 6.  
XX Hepatocyte delivery; T7; p17 rod domain.  
XX Enterobacteria phage T7.  
XX WO2004013307-A2.  
XX 12-FEB-2004.  
XX 04-AUG-2003; 2003WO-US024516.  
XX 05-AUG-2002; 2002US-0401167P.  
XX 04-AUG-2003; 2003US-00633808.  
XX (MIRU-) MIRUS CORP.  
XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Luttke J, Higgs L;  
XX Wakefield D, Sebestyen MG;  
XX WPI; 2004-203636/19.  
XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
XX a mouse, rat, monkey or human, comprising a T7 ligand attached to  
XX compound.  
XX Example 3; Page 26; 56pp; English.  
XX The present invention relates to a composition (I) for delivering a  
XX therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
XX compound. In (I), the compound comprises a drug (interferon). (I)  
XX provides better hepatocyte specificity and potentially utilizes different  
XX cellular internalization pathways which allows more flexibility in  
XX designing delivery strategies and is useful for delivering therapeutic  
XX cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
XX p17 derived peptide, such as T7 p17 rod domain (ADJ46282). The present  
XX invention is the predicted sequence of a fragment of the T7 p17 protein.  
XX Sequence 160 AA;  
XX Query Match 100.0%; Score 176; DB 8; Length 160;  
XX Best Local Similarity 100.0%; Pred. No. 9e-19;  
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
RESULT 5  
ADJ46282  
ID ADJ46282 standard; protein; 160 AA.  
XX AC ADJ46282;  
XX 06-MAY-2004 (first entry)  
XX T7 p17 protein fragment 150-289, SEQ ID 5.  
XX Hepatocyte delivery; T7; p17 rod domain.  
XX Enterobacteria phage T7.  
XX WO2004013307-A2.  
XX 12-FEB-2004.  
XX 04-AUG-2003; 2003WO-US024516.  
XX 05-AUG-2002; 2002US-0401167P.  
XX 04-AUG-2003; 2003US-00633808.  
XX (MIRU-) MIRUS CORP.

CC cellular internalization pathways which allows more flexibility in  
CC designing delivery strategies and is useful for delivering therapeutic  
CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present  
CC sequence is the predicted sequence of a fragment of the T7 p17 protein.  
XX  
SQ Sequence 309 AA;

Query Match 100.0%; Score 176; DB 8; Length 309;  
Best Local Similarity 100.0%; Pred. No. 1.1e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
DB 206 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 238  
|||||

RESULT 7  
ADJ46284  
ID ADJ46284 standard; protein; 424 AA.  
XX  
AC ADJ46284;

DT 06-MAY-2004 (first entry)

DE T7 p17 protein fragment 150-553, SEQ ID 7.

KW Hepatocyte delivery; T7; p17 rod domain.

OS Enterobacteria phage T7.

PN WO2004013307-A2.

PD 12-FEB-2004.

PF 04-AUG-2003; 2003WO-US024516.

PR 05-AUG-2002; 2002US-0401167P.

PR 04-AUG-2003; 2003US-00633808.

XX (MIRU-) MIRUS CORP.

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;

PI Wakefield D, Sebestyen MG;

DR WPI; 2004-203636/19.

XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
PT a mouse, rat, monkey or human, comprising a T7 ligand attached to  
PT compound.

PS Example 3; Page 26; 56pp; English.

XX The present invention relates to a composition (I) for delivering a  
CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
CC compound. In (I), the compound comprises a drug (interferon). (I)  
CC provides better hepatocyte specificity and potentially utilizes different  
CC cellular internalization pathways which allows more flexibility in  
CC designing delivery strategies and is useful for delivering therapeutic  
CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present  
CC sequence is the predicted sequence of a fragment of the T7 p17 protein.  
XX  
SQ Sequence 424 AA;

Query Match 100.0%; Score 176; DB 8; Length 424;  
Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
DB 57 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 89  
|||||

RESULT 8

ADJ46281  
ID ADJ46281 standard; protein; 573 AA.

XX  
AC ADJ46281;

DT 06-MAY-2004 (first entry)

DE T7 p17 protein, SEQ ID 4.

KW Hepatocyte delivery; T7; p17 rod domain.

OS Enterobacteria phage T7.

PN WO2004013307-A2.

PD 12-FEB-2004.

PF 04-AUG-2003; 2003WO-US024516.

PR 05-AUG-2002; 2002US-0401167P.

PR 04-AUG-2003; 2003US-00633808.

XX (MIRU-) MIRUS CORP.

PI Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;

PI Wakefield D, Sebestyen MG;

DR WPI; 2004-203636/19.

XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
PT a mouse, rat, monkey or human, comprising a T7 ligand attached to  
PT compound.

PS Example 3; Page 25-26; 56pp; English.

XX The present invention relates to a composition (I) for delivering a  
CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
CC compound. In (I), the compound comprises a drug (interferon). (I)  
CC provides better hepatocyte specificity and potentially utilizes different  
CC cellular internalization pathways which allows more flexibility in  
CC designing delivery strategies and is useful for delivering therapeutic  
CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). The present  
CC sequence is the predicted sequence of the full length T7 p17 protein.  
XX  
SQ Sequence 573 AA;

Query Match 100.0%; Score 176; DB 8; Length 573;  
Best Local Similarity 100.0%; Pred. No. 2.3e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||  
DB 206 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 238  
|||||

RESULT 9

ADJ46292

ID ADJ46292 standard; peptide; 33 AA.

XX  
AC ADJ46292;

DT 06-MAY-2004 (first entry)

DE T7 phage p17 protein ligand, SEQ ID 15.

KW Hepatocyte delivery; T7; p17 rod domain.

OS Enterobacteria phage T7.

XX Synthetic.

PH Key Location/Qualifiers  
FT Misc-difference 15 /note= "Wild-type residue replaced with Lys"  
XX WO2004013307-A2.  
XX 12-FEB-2004.  
XX 04-AUG-2003; 2003WO-US024516.  
XX 05-AUG-2002; 2002US-0401167P.  
PR 04-AUG-2003; 2003US-00633808.  
XX (MIRU-) MIRUS CORP.  
XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
PI Wakefield D, Sebestyen MG;  
XX WPI; 2004-203636/19.  
XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
PT a mouse, rat, monkey or human, comprising a T7 ligand attached to  
PT compound.  
XX Disclosure; Page 10; 56pp; English.  
XX The present invention relates to a composition (I) for delivering a  
CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
CC compound. In (I), the compound comprises a drug (interferon). (I)  
CC provides better hepatocyte specificity and potentially utilizes different  
CC cellular internalization pathways which allows more flexibility in  
CC designing delivery strategies and is useful for delivering therapeutic  
CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein  
CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
CC changes which do disrupt hepatocyte targeting.  
XX Sequence 33 AA;  
SQ  
Query Match 98.3%; Score 173; DB 8; Length 33;  
Best Local Similarity 97.0%; Pred. No. 2e-18;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KNESSTNATNTKQWRDETKGFRDEAKRFPKNTAG 33  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFPKNTAG 33  
RESULT 10  
ADJ46291  
ID ADJ46291 standard; peptide; 33 AA.  
XX ADJ46291;  
AC  
XX 06-MAY-2004 (first entry)  
DT  
XX T7 phase p17 protein ligand, SEQ ID 14.  
DE  
XX Hepatocyte delivery; T7; p17 rod domain.  
KW  
XX Enterobacteria phage T7.  
OS  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Misc-difference 26 /note= "Wild-type residue replaced with Arg"  
XX WO2004013307-A2.  
XX 12-FEB-2004.  
XX

PF 04-AUG-2003; 2003WO-US024516.  
XX  
XX 05-AUG-2002; 2002US-0401167P.  
PR 04-AUG-2003; 2003US-00633808.  
XX  
XX (MIRU-) MIRUS CORP.  
XX  
XX Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
PI Wakefield D, Sebestyen MG;  
XX WPI; 2004-203636/19.  
XX Composition useful for delivering a therapeutic cargo to a hepatocyte in  
PT a mouse, rat, monkey or human, comprising a T7 ligand attached to  
PT compound.  
XX Disclosure; Page 10; 56pp; English.  
XX The present invention relates to a composition (I) for delivering a  
CC therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a  
CC compound. In (I), the compound comprises a drug (interferon). (I)  
CC provides better hepatocyte specificity and potentially utilizes different  
CC cellular internalization pathways which allows more flexibility in  
CC designing delivery strategies and is useful for delivering therapeutic  
CC cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7  
CC p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-  
CC ADJ46313 are synthetic peptides derived from the T7 phase p17 protein  
CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not  
CC disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid  
CC changes which do disrupt hepatocyte targeting.  
XX Sequence 33 AA;  
SQ  
Query Match 98.3%; Score 173; DB 8; Length 33;  
Best Local Similarity 97.0%; Pred. No. 2e-18;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KNESSTNATNTKQWRDETKGFRDEAKRFPKNTAG 33  
DB 1 KNESSTNATNTKQWRDETKGFRDEAKRFPKNTAG 33  
RESULT 11  
ADJ46293  
ID ADJ46293 standard; peptide; 33 AA.  
XX  
XX ADJ46293;  
AC  
XX 18-NOV-2004 (first entry)  
DT  
XX Bacteriophage T7 cholesterol modified cell targeting peptide MC1054.  
DE  
XX Post-synthetic modification; nuclease; siRNA; microRNA; cell delivery;  
KW small interfering RNA; cell targeting peptide; cholesterol.  
XX  
XX Enterobacteria phage T7.  
OS  
XX  
XX Key Location/Qualifiers  
FT Modified-site 1 /note= "Lys modified with cholesterol chloroformate"  
FT  
XX US2004167090-A1.  
XX 26-AUG-2004.  
XX  
XX 19-FEB-2004; 2004US-00782075.  
XX  
XX 21-FEB-2003; 2003US-0448789P.  
PR 18-MAR-2003; 2003US-0455724P.  
XX  
XX (MONA/) MONAHAN S D.  
PA (BUDK/) BUDKER V G.  
PA (NADE/) NADER L.  
PA



therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-ADJ46313 are synthetic peptides derived from the T7 phage p17 protein ligand, where ADJ46291-ADJ46301 have amino acid changes which do not disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid changes which do disrupt hepatocyte targeting.

XX Sequence 33 AA;

Query Match 96.6%; Score 170; DB 8; Length 33;  
Best Local Similarity 97.0%; Pred. No. 5.6e-18;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 14  
ADJ46300  
ID ADJ46300 standard; peptide; 33 AA.  
XX AC ADJ46300;  
DT 06-MAY-2004 (first entry)  
DE T7 phage p17 protein ligand, SEQ ID 23.  
KW Hepatocyte delivery; T7; p17 rod domain.  
XX Enterobacteria phage T7.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT Misc-difference 26 /note= "Wild-type residue replaced with Ornithine"  
XX WO2004013307-A2.  
XX 12-FEB-2004.

04-AUG-2003; 2003WO-US024516.  
05-AUG-2002; 2002US-0401167P.  
04-AUG-2003; 2003US-00633808.  
(MIRU-) MIRUS CORP.  
Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
Wakefield D, Sebestyen MG;  
WPI; 2004-203636/19.  
Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to compound.  
Disclosure; Page 10; 56pp; English.

The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-ADJ46313 are synthetic peptides derived from the T7 phage p17 protein

CC ligand, where ADJ46291-ADJ46301 have amino acid changes which do not disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid changes which do disrupt hepatocyte targeting.  
XX Sequence 33 AA;

Query Match 96.6%; Score 170; DB 8; Length 33;  
Best Local Similarity 97.0%; Pred. No. 5.6e-18;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

Db 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33  
|||||

RESULT 15  
ADJ46304  
ID ADJ46304 standard; peptide; 33 AA.  
XX AC ADJ46304;  
DT 06-MAY-2004 (first entry)  
DE T7 phage p17 protein ligand-related peptide, SEQ ID 27.  
KW Hepatocyte delivery; T7; p17 rod domain.  
XX Enterobacteria phage T7.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT Misc-difference 12 /note= "Wild-type residue replaced with Arg"  
FT Misc-difference 19 /note= "Wild-type residue replaced with Arg"  
FT Misc-difference 26 /note= "Wild-type residue replaced with Arg"  
XX WO2004013307-A2.  
XX 12-FEB-2004.  
XX 04-AUG-2003; 2003WO-US024516.  
XX 05-AUG-2002; 2002US-0401167P.  
XX 04-AUG-2003; 2003US-00633808.  
(MIRU-) MIRUS CORP.  
Sokoloff AV, Wong S, Wolff JA, Monahan SD, Ludtke J, Higgs L;  
Wakefield D, Sebestyen MG;  
WPI; 2004-203636/19.  
Composition useful for delivering a therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human, comprising a T7 ligand attached to compound.  
Disclosure; Page 10; 56pp; English.

The present invention relates to a composition (I) for delivering a therapeutic cargo to a hepatocyte, comprising a T7 ligand attached to a compound. In (I), the compound comprises a drug (interferon). (I) provides better hepatocyte specificity and potentially utilizes different cellular internalization pathways which allows more flexibility in designing delivery strategies and is useful for delivering therapeutic cargo to a hepatocyte in a mouse, rat, monkey or human. The T7 ligand T7 p17 derived peptide, such as T7 p17 rod domain (ADJ46278). ADJ46291-ADJ46313 are synthetic peptides derived from the T7 phage p17 protein ligand, where ADJ46291-ADJ46301 have amino acid changes which do not disrupt hepatocyte targeting, and ADJ46302-ADJ46313 have amino acid changes which do disrupt hepatocyte targeting.

SQ Sequence 33 AA;

Query Match 94.9%; Score 167; DB 8; Length 33;  
Best Local Similarity 90.9%; Pred. No. 1.6e-17;  
Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESTNATNTKQWRDETKGFRDEAKRPFKNTAG 33  
|||||:|||||:|||||:|||||:|||||  
Db 1 KNESTNATNTQWRDETRGFRDEARRPFKNTAG 33

Search completed: March 30, 2005, 14:33:50  
Job time : 171 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 30, 2005, 14:15:25 ; Search time 189 Seconds  
(without alignments)  
89.411 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: 1 KNESSNTATNTKQWRDETKGFRDEAKRPKNTAG 33

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 176   | 100.0       | 553    | 1 VTFF BPT7 | P03748 bacterioph  |
| 2          | 176   | 100.0       | 553    | 2 Q8LTX6    | Q8LTX6 bacterioph  |
| 3          | 170   | 96.6        | 553    | 2 Q6WY17    | Q6WY17 bacterioph  |
| 4          | 170   | 96.6        | 553    | 2 Q6WY69    | Q6WY69 bacterioph  |
| 5          | 168   | 95.5        | 553    | 2 Q6WYC3    | Q6WYC3 bacterioph  |
| 6          | 168   | 95.5        | 553    | 2 Q6WYH2    | Q6WYH2 bacterioph  |
| 7          | 166   | 94.3        | 553    | 2 Q8LTX0    | Q8LTX0 bacterioph  |
| 8          | 164   | 93.2        | 553    | 2 Q8LTX1    | Q8LTX1 bacterioph  |
| 9          | 159   | 90.3        | 553    | 2 Q8LTX3    | Q8LTX3 bacterioph  |
| 10         | 157   | 89.2        | 553    | 2 Q8LTX7    | Q8LTX7 bacterioph  |
| 11         | 157   | 89.2        | 553    | 2 Q8LTX9    | Q8LTX9 bacterioph  |
| 12         | 152   | 86.4        | 553    | 2 Q8LTX5    | Q8LTX5 bacterioph  |
| 13         | 152   | 86.4        | 553    | 2 Q8LTX7    | Q8LTX7 bacterioph  |
| 14         | 152   | 86.4        | 553    | 2 Q8LTX8    | Q8LTX8 bacterioph  |
| 15         | 152   | 86.4        | 553    | 2 Q8LTX7    | Q8LTX7 bacterioph  |
| 16         | 152   | 86.4        | 553    | 2 Q8LTX1    | Q8LTX1 bacterioph  |
| 17         | 152   | 86.4        | 553    | 2 Q8LTX2    | Q8LTX2 bacterioph  |
| 18         | 151   | 85.8        | 553    | 2 Q8LTX9    | Q8LTX9 bacterioph  |
| 19         | 151   | 85.8        | 553    | 2 Q8LTX8    | Q8LTX8 bacterioph  |
| 20         | 151   | 85.8        | 553    | 2 Q8LTX3    | Q8LTX3 bacterioph  |
| 21         | 151   | 85.8        | 553    | 2 Q8LTX4    | Q8LTX4 bacterioph  |
| 22         | 151   | 85.8        | 553    | 2 Q8LTX5    | Q8LTX5 bacterioph  |
| 23         | 151   | 85.8        | 553    | 2 Q8LTX8    | Q8LTX8 bacterioph  |
| 24         | 147   | 83.5        | 553    | 2 Q8LTX9    | Q8LTX9 bacterioph  |
| 25         | 147   | 83.5        | 553    | 2 Q8LTX0    | Q8LTX0 bacterioph  |
| 26         | 146   | 83.0        | 553    | 2 Q8LTX4    | Q8LTX4 bacterioph  |
| 27         | 146   | 83.0        | 553    | 2 Q8LTX0    | Q8LTX0 bacterioph  |
| 28         | 146   | 83.0        | 557    | 1 VTFF BPT3 | P10308 bacterioph  |
| 29         | 146   | 83.0        | 558    | 2 Q8W5T8    | Q8W5T8 bacterioph  |
| 30         | 146   | 83.0        | 558    | 2 Q8S8J8    | Q8S8J8 yersinia pe |
| 31         | 144   | 81.8        | 553    | 2 Q8LTX2    | Q8LTX2 bacterioph  |

|    |      |      |      |          |                    |
|----|------|------|------|----------|--------------------|
| 32 | 143  | 81.2 | 553  | 2 Q8LTX6 | Q8LTX6 bacterioph  |
| 33 | 143  | 81.2 | 553  | 2 Q8LTX2 | Q8LTX2 bacterioph  |
| 34 | 67   | 38.1 | 1647 | 2 Q7RRX4 | Q7RRX4 plasmodium  |
| 35 | 61   | 34.7 | 879  | 2 Q41010 | Q41010 pium sativ  |
| 36 | 61   | 34.7 | 879  | 2 Q7DLK2 | Q7DLK2 pium sativ  |
| 37 | 61   | 34.7 | 1469 | 2 Q9LXK1 | Q9LXK1 pium sativ  |
| 38 | 60   | 34.1 | 604  | 2 Q8A3N2 | Q8A3N2 bacteroides |
| 39 | 60   | 34.1 | 1292 | 2 Q9LDN0 | Q9LDN0 arabidopsis |
| 40 | 60   | 34.1 | 1662 | 2 Q23274 | Q23274 arabidopsis |
| 41 | 57   | 32.4 | 186  | 2 Q8YLY6 | Q8YLY6 anabaena sp |
| 42 | 57   | 32.4 | 509  | 2 Q8YKZ2 | Q8YKZ2 anabaena sp |
| 43 | 56.5 | 32.1 | 1097 | 2 Q13592 | Q13592 saccharomyc |
| 44 | 56   | 31.8 | 1785 | 2 Q6FS79 | Q6FS79 candida gla |
| 45 | 55.5 | 31.5 | 552  | 2 Q8ID98 | Q8ID98 plasmodium  |

#### ALIGNMENTS

##### RESULT 1

VTFF BPT7 STANDARD; PRT; 553 AA.  
AC P03748;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tail fiber protein.  
GN Name=17;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83241725; PubMed=6864790;  
RA Dunn J.J., Studier F.W.;  
RT "Complete nucleotide sequence of bacteriophage T7 DNA and the  
RT locations of T7 genetic elements.";  
RL J. Mol. Biol. 166:477-535(1983).  
CC -----  
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CC -----  
DR EMBL; V01146; CAA24435.1; -;  
DR PIR; A04373; TLBPP7.  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage\_T7\_tail\_1.  
KW Fiber protein.  
SQ SEQUENCE 553 AA; 61572 MW; 98B82DFADBDEAC1 CRC64;

Query Match 100.0%; Score 176; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 1.3e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy : 1 KNESSNTATNTKQWRDETKGFRDEAKRPKNTAG 33  
Db : 186 KNESSNTATNTKQWRDETKGFRDEAKRPKNTAG 218

##### RESULT 2

Q8LTX6 PRELIMINARY; PRT; 553 AA.  
ID Q8LTX6  
AC Q8LTX6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;

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OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RL experimental lineage of bacteriophage T7.";
DR EMBL; AF419438; AAM43534.1; -
DR InterPro; IPR005604; T7 tail fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 61560 MW; 11A394FADBDBEAD1 CRC64;

Query Match 100.0%; Score 176; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
DB 186 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

RESULT 3
Q6WY17 PRELIMINARY; PRT; 553 AA.
AC Q6WY17;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Gene 17.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokya D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RL viral genome.";
DR EMBL; AY264778; AAP34164.1; -
DR InterPro; IPR005604; T7 tail fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 61833 MW; ECF0426C8E74CC13 CRC64;

Query Match 96.6%; Score 170; DB 2; Length 553;
Best Local Similarity 97.0%; Pred. No. 8.8e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
DB 186 KNEFSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

RESULT 4
Q6WY69 PRELIMINARY; PRT; 553 AA.
AC Q6WY69;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Gene 17.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokya D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RL viral genome.";
DR EMBL; AY264778; AAP34164.1; -
DR InterPro; IPR005604; T7 tail fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 61833 MW; ECF0426C8E74CC13 CRC64;

Query Match 96.6%; Score 170; DB 2; Length 553;
Best Local Similarity 97.0%; Pred. No. 8.8e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
DB 186 KNEFSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

RESULT 5
Q6WY17 PRELIMINARY; PRT; 553 AA.
AC Q6WY17;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Gene 17.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokya D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RL viral genome.";
DR EMBL; AY264778; AAP34058.1; -
DR InterPro; IPR005604; T7 tail fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 61788 MW; 8E754373B814980C CRC64;

Query Match 95.5%; Score 168; DB 2; Length 553;
Best Local Similarity 97.0%; Pred. No. 1.7e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
DB 186 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

RESULT 6
Q6WYH2 PRELIMINARY; PRT; 553 AA.
AC Q6WYH2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Gene 17.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokya D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RL viral genome.";
DR EMBL; AY264775; AAP34009.1; -
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.

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RA Bull J.J., Badgett M.R., Rokya D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RL viral genome.";
RL J. Mol. Evol. 57:241-248(2003).
DR EMBL; AY264777; AAP34112.1; -
DR InterPro; IPR005604; T7 tail fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 61787 MW; 58F0426D9A74CC11 CRC64;

Query Match 96.6%; Score 170; DB 2; Length 553;
Best Local Similarity 97.0%; Pred. No. 8.8e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
DB 186 KNEFSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

RESULT 5
Q6WY17 PRELIMINARY; PRT; 553 AA.
AC Q6WY17;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Gene 17.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokya D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RL viral genome.";
DR EMBL; AY264776; AAP34058.1; -
DR InterPro; IPR005604; T7 tail fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 61788 MW; 8E754373B814980C CRC64;

Query Match 95.5%; Score 168; DB 2; Length 553;
Best Local Similarity 97.0%; Pred. No. 1.7e-14;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 33
DB 186 KNESSTNATNTKQWRDETKGFRDEAKRFKNTAG 218

RESULT 6
Q6WYH2 PRELIMINARY; PRT; 553 AA.
AC Q6WYH2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Gene 17.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokya D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RL viral genome.";
DR EMBL; AY264775; AAP34009.1; -
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.

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SQ SEQUENCE 553 AA; 61832 MW; CE2632DB5E36B85F CRC64;  
Query Match 95.5%; Score 168; DB 2; Length 553;  
Best Local Similarity 97.0%; Pred. No. 1.7e-14;  
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 33  
|||||  
DB 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTAG 218

RESULT 7  
QBLTXO PRELIMINARY; PRT; 553 AA.  
AC QBLTXO;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7.";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419444; AAM43540.1; -;  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage T7 tail; 1.  
SQ SEQUENCE 553 AA; 61829 MW; 8B995AA3956CDEE9 CRC64;

Query Match 94.3%; Score 166; DB 2; Length 553;  
Best Local Similarity 96.9%; Pred. No. 3.1e-14;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 32  
|||||  
DB 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 217

RESULT 8  
QBLTX1 PRELIMINARY; PRT; 553 AA.  
AC QBLTX1;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7.";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419443; AAM43539.1; -;  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage T7 tail; 1.  
SQ SEQUENCE 553 AA; 61753 MW; ADAB0C4B2E5BDB16 CRC64;

Query Match 93.2%; Score 164; DB 2; Length 553;  
Best Local Similarity 96.9%; Pred. No. 5.9e-14;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 32  
|||||  
DB 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 217

RESULT 9  
QBLTU3 PRELIMINARY; PRT; 553 AA.  
AC QBLTU3;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7.";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419510; AAM43606.1; -;  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage T7 tail; 1.  
SQ SEQUENCE 553 AA; 62061 MW; E32BB0B02ADAF22 CRC64;

Query Match 90.3%; Score 159; DB 2; Length 553;  
Best Local Similarity 93.8%; Pred. No. 2.9e-13;  
Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 32  
|||||  
DB 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 217

RESULT 10  
QBLTW7 PRELIMINARY; PRT; 553 AA.  
AC QBLTW7;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE Tail fiber protein.  
GN Name=17.0;  
OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an experimental lineage of bacteriophage T7.";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419447; AAM43543.1; -;  
DR InterPro; IPR005604; T7 tail fibre.  
DR Pfam; PF03906; Phage T7 tail; 1.  
SQ SEQUENCE 553 AA; 61952 MW; FDBF4FB200825A99 CRC64;

Query Match 89.2%; Score 157; DB 2; Length 553;  
Best Local Similarity 93.8%; Pred. No. 5.4e-13;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 32  
|||||  
DB 186 KNESSTNATNTKQWRDETKGFRDEAKRPNKNTA 217

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RESULT 11
Q8LTW9
ID Q8LTW9 PRELIMINARY; PRT; 553 AA.
AC Q8LTW9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RT experimental lineage of bacteriophage T7.";
RL Genetics 161:11-20(2002).
DR EMBL; AF419445; AAM43541.1; -.
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 61805 MW; 882675FB6B09895F CRC64;

Query Match 89.2%; Score 157; DB 2; Length 553;
Best Local Similarity 93.8%; Pred. No. 5.4e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTA 32
Db 186 KDESSTNATNTKQWRDEIKDFRDEAKRFKNTA 217

RESULT 12
Q8LTU5
ID Q8LTU5 PRELIMINARY; PRT; 553 AA.
AC Q8LTU5;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RT experimental lineage of bacteriophage T7.";
RL Genetics 161:11-20(2002).
DR EMBL; AF419508; AAM43604.1; -.
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 62184 MW; 66A0BC1246E4E421 CRC64;

Query Match 86.4%; Score 152; DB 2; Length 553;
Best Local Similarity 90.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTA 32
Db 186 KDESSTNATNTKQWRDEIKDFRDEAKRFKNTA 217

RESULT 13
Q8LTU7
ID Q8LTU7 PRELIMINARY; PRT; 553 AA.
AC Q8LTU7;

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DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RT experimental lineage of bacteriophage T7.";
RL Genetics 161:11-20(2002).
DR EMBL; AF419506; AAM43602.1; -.
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 62092 MW; E0E509A5FAADA3EC CRC64;

Query Match 86.4%; Score 152; DB 2; Length 553;
Best Local Similarity 90.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTA 32
Db 186 KDESSTNATNTKQWRDEIKDFRDEAKRFKNTA 217

RESULT 14
Q8LTU8
ID Q8LTU8 PRELIMINARY; PRT; 553 AA.
AC Q8LTU8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013848; PubMed=12019219;
RA Hahn M.W., Rausher M.D., Cunningham C.W.;
RT "Distinguishing between selection and population expansion in an
RT experimental lineage of bacteriophage T7.";
RL Genetics 161:11-20(2002).
DR EMBL; AF419505; AAM43601.1; -.
DR InterPro; IPR005604; T7_tail_fibre.
DR Pfam; PF03906; Phage_T7_tail; 1.
SQ SEQUENCE 553 AA; 62303 MW; 5868AAE51F700CC CRC64;

Query Match 86.4%; Score 152; DB 2; Length 553;
Best Local Similarity 90.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNESSTNATNTKQWRDETKGFRDEAKRFKNTA 32
Db 186 KDESSTNATNTKQWRDEIKDFRDEAKRFKNTA 217

RESULT 15
Q8LTXT7
ID Q8LTXT7 PRELIMINARY; PRT; 553 AA.
AC Q8LTXT7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Tail fiber protein.
GN Name=17.0;

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OS Bacteriophage T7.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
OC T7-like viruses.  
OX NCBI\_TaxID=10760;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22013848; PubMed=12019219;  
RA Hahn M.W., Rausher M.D., Cunningham C.W.;  
RT "Distinguishing between selection and population expansion in an  
RT experimental lineage of bacteriophage T7";  
RL Genetics 161:11-20(2002).  
DR EMBL; AF419437; AAM43533.1; -  
DR InterPro; IPR005604; T7\_tail\_fibre.  
DR Pfam; PF03906; Phage\_T7\_tail; 1.  
SQ SEQUENCE 553 AA; 62029 MW; 88C653CDF5C4FEB9 CRC64;

Query Match 86.4%; Score 152; DB 2; Length 553;  
Best Local Similarity 90.6%; Pred. No. 2.6e-12;  
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 KNESSTNATNTKQWRDETKGFRDEAKRPFKNTA 32  
|:|||||  
Db 186 KDESSTNATNTKQWRDEIKDFRDEAKRPFKNTA 217

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Job time : 190 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 14:27:07 ; Search time 43 Seconds  
(without alignments)  
73.841 Million cell updates/sec

Title: US-10-633-808-1

Perfect score: 176

Sequence: 1 KNESSTATNTKQWRDETKGFRDEAKRFPKNTAG 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 176   | 100.0       | 553    | 1 TLBPF7 | tail fiber protein |
| 2          | 146   | 83.0        | 557    | 1 TLBPT3 | tail fiber protein |
| 3          | 61    | 34.7        | 879    | 2 S49910 | chloroplast outer  |
| 4          | 60    | 34.1        | 1662   | 1 H71402 | probable kinesin - |
| 5          | 57    | 32.4        | 186    | 2 A2450  | hypothetical prote |
| 6          | 57    | 32.4        | 509    | 2 A2496  | transposase alr714 |
| 7          | 56.5  | 32.1        | 3079   | 1 RGBY12 | probable GTPase-ac |
| 8          | 55    | 31.2        | 466    | 2 T07404 | probable glucosylt |
| 9          | 54    | 30.7        | 346    | 2 G87440 | rod shape-determ   |
| 10         | 53    | 30.1        | 167    | 2 S46656 | ubiquitin-protein  |
| 11         | 53    | 30.1        | 880    | 2 T48477 | hypothetical prote |
| 12         | 52    | 29.5        | 69     | 2 A82489 | cold shock DNA-bin |
| 13         | 52    | 29.5        | 169    | 2 T02943 | ubiquitin-conjugat |
| 14         | 51.5  | 29.3        | 174    | 2 A26666 | conserved hypotet  |
| 15         | 51.5  | 29.3        | 192    | 2 B97448 | immunoreactive 14K |
| 16         | 51    | 29.0        | 166    | 2 S71209 | ubiquitin-protein  |
| 17         | 51    | 29.0        | 573    | 2 F81313 | peptidase (M3 fami |
| 18         | 50.5  | 28.7        | 648    | 2 A83792 | acetyl-CoA synthet |
| 19         | 50    | 28.4        | 136    | 2 A96905 | uncharacterized sm |
| 20         | 50    | 28.4        | 476    | 2 T03745 | glucosyltransferas |
| 21         | 50    | 28.4        | 751    | 2 B87391 | TonB-dependent rec |
| 22         | 50    | 28.4        | 960    | 2 AF1940 | isoleucyl-tRNA syn |
| 23         | 50    | 28.4        | 2481   | 2 D30011 | FmtB protein [impo |
| 24         | 50    | 28.4        | 3328   | 2 T30835 | breast cancer tumo |
| 25         | 50    | 28.4        | 3329   | 2 T42205 | breast cancer susc |
| 26         | 50    | 28.4        | 3329   | 2 T30904 | breast cancer tumo |
| 27         | 49    | 27.8        | 70     | 2 E32399 | cold shock domain  |
| 28         | 49    | 27.8        | 298    | 2 S50735 | hypothetical prote |
| 29         | 49    | 27.8        | 336    | 2 G81152 | probable DNA-bind  |

30 49 27.8 453 2 JE0155 mitochondrial inne  
31 49 27.8 615 2 T06108 hypothetical prote  
32 48.5 27.6 112 2 T06732 hypothetical prote  
33 48.5 27.6 282 2 B81264 probable DNA ligas  
34 48.5 27.6 604 2 A84753 hypothetical prote  
35 48.5 27.6 774 2 A10106 conserved hypotet  
36 48.5 27.6 2663 1 S28261 centromere protein  
37 48 27.3 210 2 T06656 hypothetical prote  
38 48 27.3 476 2 T03747 glucosyltransferas  
39 48 27.3 549 2 T40692 hypothetical prote  
40 48 27.3 1222 2 G59100 hypothetical prote  
41 48 27.3 2543 2 T31687 surface antigen - P  
42 48 27.3 2677 2 A38194 desmoplakin I - hu  
43 47.5 27.0 641 1 A41932 fibrinogen alpha-I  
44 47.5 27.0 2206 2 JCS280 voltage-dependent  
45 47 26.7 166 2 T45703 ubiquitin-protein

#### ALIGNMENTS

##### RESULT 1

TLBPF7

tail fiber protein - phase T7

C:Species: phase T7

C:Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004

C:Accession: A04373; S42333

R:Dunn, J.J.; Thompson, K.

submitted to the Nucleic Acid Sequence Database, September 1982

A:Reference number: A94615

A:Accession: A04373

A:Molecule type: DNA

A:Residues: 1-553 <DUN>

A:Cross-references: UNIPROT:P03748

R:Dunn, J.J.; Studier, F.W.

J. Mol. Biol. 166, 477-535, 1983

A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 genes

A:Reference number: S42283; MUID:83241725; PMID:6864790

A:Accession: S42333

A:Molecule type: DNA

A:Residues: 1-553 <DUN>

A:Cross-references: EMBL:V01146; NID:9431187; PIDN:CAA24435.1; PID:g15611

A:Note: the authors did not translate the codon for residue 1

C:Genetics:

A:Gene: 17

A:Map position: 86.70-90.85

C:Superfamily: phase T7 tail fiber protein

C:Keywords: tail fiber

Query Match 100.0%; Score 176; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 7.5e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNESSTATNTKQWRDETKGFRDEAKRFPKNTAG 33

|||||  
Db 186 KNESSTATNTKQWRDETKGFRDEAKRFPKNTAG 218

##### RESULT 2

TLBPT3

tail fiber protein - phase T3

C:Species: phase T3

A:Note: host Escherichia coli

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

C:Accession: A23476

R:Yamada, M.; Fujisawa, H.; Kato, H.; Hamada, K.; Minagawa, T.

Virology 151, 350-361, 1986

A:Title: Cloning and sequencing of the genetic right end of bacteriophage T3 DNA.

A:Reference number: A94339; MUID:86209997; PMID:3010556

A:Accession: A23476

A:Molecule type: DNA

A:Residues: 1-557 <YAM>

A:Cross-references: UNIPROT:P10308; GB:M14784; NID:g215810; PIDN:AAA92523.1; PID:g215811



F/1701-1910/Domain: ras-specific GAP catalytic domain homology <GAP>  
F/1842-1858/Domain: transmembrane #status predicted <TM3>  
F/2318-2334/Domain: transmembrane #status predicted <TM4>  
F/2562-2578/Domain: transmembrane #status predicted <TM5>

[illegible]

F/1701-1910/Domain: ras-specific GAP catalytic domain homology <GAP>  
F/1842-1858/Domain: transmembrane #status predicted <TM3>  
F/2318-2334/Domain: transmembrane #status predicted <TM4>  
F/2562-2578/Domain: transmembrane #status predicted <TM5>

RESULT 12

AB2489  
cold shock DNA-binding domain protein VCA0184 [imported] - Vibrio cholerae (strain N1696)

C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: AB2489  
R;Reideldberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
Chardon, D.; Emwolaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.;  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: AB2035; MUID:20406833; PMID:10952301  
A;Accession: AB2489  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-69 <HEI>  
A;Cross-references: UNIPROT:Q9KMY2; GB:AE004359; GB:AE003853; NID:9657575; PIDN:AAF9609  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VCA0184  
A;Map position: 2  
C;Superfamily: cold shock protein, cspA type; cold shock domain homology

Query Match 29.5%; Score 52; DB 2; Length 69;  
Best Local Similarity 58.8%; Pred. No. 3.7;  
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 STNATNTKQWRDETKGF 21  
||| : : : : :  
DB 2 STPVTGTVKWFNETKGF 18

RESULT 13

T02943  
ubiquitin-conjugating enzyme - maize

N;Alternate names: ubiquitin carrier protein  
C;Species: Zea mays (maize)  
C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C;Accession: T02943  
R;de Vries, A.; Cordts, S.; Dresselhaus, T.  
Plant Physiol. 118, 1101, 1998  
A;Title: Molecular Characterization of a cDNA Encoding an Ubiquitin Carrier Protein (UBC)

A;Reference number: Z14787; MUID:99105148; PMID:9890811  
A;Accession: T02943  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-169 <DEV>  
A;Cross-references: UNIPROT:Q24560; EMBL:AJ002959; PIDN:CAA05772.1  
C;Superfamily: human ubiquitin-protein ligase E2

Query Match 29.5%; Score 52; DB 2; Length 169;  
Best Local Similarity 30.8%; Pred. No. 9.7;  
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 NESSTNATNTKQWRDETKGFRDEAKR 27  
||| : : : : :  
DB 135 DESPANIEAAKWRQREDFKKKVR 160

RESULT 14

AD2666  
conserved hypothetical protein Atu0730 [imported] - Agrobacterium tumefaciens (strain C5)

C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AD2666  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.



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